

SID4

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RESULT      2
S57294
LOCUS       S57294          250 bp      DNA          MAM          28-JUN-1993
DEFINITION  {D-loop region} [cattle, Mitochondrial, 250 nt].
ACCESSION   S57294
VERSION     S57294.1  GI:298691
KEYWORDS     .
SOURCE      cow.
  ORGANISM   Mitochondrion Bos taurus
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
              Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 250)
AUTHORS     Madsen,C.S., Ghivizzani,S.C. and Hauswirth,W.W.
TITLE       Protein binding to a single termination-associated sequence in the
              mitochondrial DNA D-loop region
JOURNAL     Mol. Cell. Biol. 13 (4), 2162-2171 (1993)
MEDLINE     93204962
REMARK      GenBank staff at the National Library of Medicine created this
              entry [NCBI gibbsq 127635] from the original journal article.
              This sequence comes from Fig. 2.
COMMENT     Sequence is identical to previously published sequence with
              exception of an A-to-G transition at position 16079.
FEATURES             Location/Qualifiers
     source           1..250
                     /organism="Bos taurus"
                     /organelle="mitochondrion"
                     /db_xref="taxon:9913"
BASE COUNT      92 a      46 c      34 g      78 t
ORIGIN

      Query Match          100.0%;  Score 46;  DB 3;  Length 250;
      Best Local Similarity 100.0%;  Pred. No. 1.8e-08;
      Matches 46;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1 attatatgccccatgcatataagcaagtacatgacctctatagcag 46
      ||||||||||||||||||||||||||||||||||||||||||||
Db      73 ATTATATGCCCCATGCATATAAGCAAGTACATGACCTCTATAGCAG 118

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-continued

Ser	Phe	Asp	Leu	Leu	Leu	Ser	Ser	Lys	Asn	Gly	Val	Ala	Ala	Phe	His
65					70					75					80
Ala	Phe	Leu	Lys	Thr	Glu	Phe	Ser	Glu	Glu	Asn	Leu	Glu	Phe	Trp	Leu
			85						90					95	
Ala	Cys	Glu	Glu	Phe	Lys	Lys	Ile	Arg	Ser	Ala	Thr	Lys	Leu	Ala	Ser
		100						105					110		
Arg	Ala	His	Gln	Ile	Phe	Glu	Glu	Phe	Ile	Cys	Ser	Glu	Ala	Pro	Lys
		115				120						125			
Glu	Val	Asn	Ile	Asp	His	Glu	Thr	Arg	Glu	Leu	Thr	Arg	Met	Asn	Leu
	130					135					140				
Gln	Thr	Ala	Thr	Ala	Thr	Cys	Phe	Asp	Ala	Ala	Gln	Gly	Lys	Thr	Arg
145				150						155					160
Thr	Leu	Met	Glu	Lys	Asp	Ser	Tyr	Pro	Arg	Phe	Leu	Lys	Ser	Pro	Ala
			165					170						175	
Tyr	Arg	Asp	Leu	Ala	Ala	Gln	Ala	Ser	Ala	Ala	Ser	Ala	Thr	Leu	Ser
		180					185							190	
Ser	Cys	Ser	Leu	Asp	Gln	Pro	Ser	His	Thr						
	195					200		202							

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 171..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTTAGACCA	ACTCAGGAAA	TAGGTGCACA	CAAGCAAACC	ATGTGGTTAA	AGCCTTTGGA	60
ACTGCTTTGA	GCAAAGCTGT	AGCTGATTTC	ACAAAATCAT	CTGCAAAACC	AGATTCTTAA	120
CACCTCCCTG	CTGTGTATCT	CATTCTGCT	GATGTGTGGT	GCTTCATAAG	ATG GGG	176
ACG TTA AGC	ATG CAG CAA	CTA CAG TCA	TTT GTT CTC	AGA GGT CTG	GAC	224
CAA AGA GAA	ACA AGA AAA	GCT GGA GTC	ACA CTA CCA	AAG GCC GAA	GCT	272
GAG CAA CAG	AGC TCT GGA	GTC AGC TGC	CTG GGT TCA	GCA TGC AGC	GCT	320
GCC GTG GAC	GAT CTG TCT	CTC TTG CAT	ATA T GACTTACCAG	TTTTACTTTC		371
AGTCTCTCCA	TTTCTAATTA	AATGAGATGC	AGAAATGCTG	GTGCCTTGCT	ATGATGTTTG	431
CAGTTATTAT	TTCTAGGAAA	AAAAATATTA	TTGTTACTCA	GTATCTGGTC	TAGCTACTTG	491
GACAACTGGA	CTATCCCCCT	CCTTCAAGG	GAGGGCAAAG	CATTTCAGAA	AAGAACTAAG	551
TGCTATTTCT	CTGCTTCAGG	AATGTCTCCC	GTATGTAAAA	GAATGTGGCT	TCAGGGAGTA	611
GCATGTGTTG	TAAAGGTGGA	TGGGTCTAAC	TTCATGGACA	GCTCTGACAT	CCACTAGCTA	671
TGCCACCTGA	TGCAAAACCAC	TGGGCTGTC	TGCAGTTTCG	TTTATCTTTC	TGGAATTGGT	731
AATAACAACC	ACCTGGCAAG	ATCACTGTTA	TGAATACGGA	GGATCAAAGT	TGTGAAGTTA	791
TTTGTAAAG	TGAAATGTTT	TGAAAAATGG	ATTTTAACAG	TGTGAGCGAA	AAGTAGATT	851
TTGACATTTA	TCAAGAGTTC	AGCTAATGAA	AACAAGTATG	GATAATAGTT	ACATAGAACT	911
GTCTACTTTA	CTCAGTACTT	TAGCATATGC	TATTATATTT	AATCTTCTTA	AAAAGTAGGA	971
AATTATACAA	GCCATGTATT	GATATTATTG	TGGTGGTTGT	CGTTCCTCAAT	TACACACTGA	1031